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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/925,576	08/09/2001	Carsten Andersen	10004.204-US	2881

25908 7590 07/18/2005

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NEW YORK, NY 10110

EXAMINER	
RAO, MANJUNATH N	

ART UNIT	PAPER NUMBER
1652	

DATE MAILED: 07/18/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/925,576	ANDERSEN ET AL.	
	Examiner	Art Unit	
	Manjunath N. Rao, Ph.D.	1652	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *11 May 2005*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *25-30,36,43,50 and 57* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *25-30,36,43,50 and 57* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *Sequence alignment*.

DETAILED ACTION

Claims 25-30, 36, 43, 50, 57, 58 are currently pending and are present for examination.

Applicants' amendments and arguments filed on 5-11-05, have been fully considered and are deemed to be persuasive to overcome the rejections previously applied. Rejections and/or objections not reiterated from previous office actions are hereby withdrawn. Specifically, Examiner has withdrawn the objection to specification and rejections under 35 U.S.C. 112, 1st paragraph (biological deposit requirement) and 2nd paragraph in view of claim amendments and claim cancellations.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 26-29 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claims 26-29 recite the phrase "corresponding to". The metes and bounds of the above phrase is not clear to the Examiner. It is not clear to the Examiner whether the phrase, for example, "corresponding to R118K" means the amino acid is at position 118 in SEQ ID NO:12 is an arginine which is changed to lysine or whether it refers to some other "arginine" amino acid at a different position which applicant claims as "corresponding to arginine at position 118". If it is the latter, then without a specific definition as to how one skilled in the art can identify the amino acid corresponding to 118 it will be impossible for the Examiner to do a meaningful

search. The same applies to other amino acid positions 320 and 458. Examiner suggests direct reference to the position number without the phrase "corresponding to".

In response to the previous Office action, applicant does not appear to have addressed specifically the above rejection. However, since the amendments and cancellations made does not rectify claims 26-29, Examiner continues to maintain the above rejection.

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 25-30, 36, 43, 50, 57, 58, are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for a variant amylase enzyme of SEQ ID NO:12 wherein the variant comprises an alteration selected from the group of alterations to amino acid at positions 118, 320 or 458 and wherein the alteration specifically comprises replacing the amino acid at said positions with lysine (K), does not reasonably provide enablement for variant amylase enzyme wherein the variant comprises a polypeptide having at least 80%, 90%, 95% or 97% homology with SEQ ID NO: 12, as well as an alteration selected from the group of alterations corresponding to amino acid at position 118, 320 or 458 and wherein the alteration specifically comprises replacing the amino acid at said positions with lysine (K). The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make the invention commensurate in scope with these claims.

Factors to be considered in determining whether undue experimentation is required, are summarized in *In re Wands* (858 F.2d 731, 8 USPQ 2nd 1400 (Fed. Cir. 1988)) as follows: (1)

the quantity of experimentation necessary, (2) the amount of direction or guidance presented, (3) the presence or absence of working examples, (4) the nature of the invention, (5) the state of the prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the claim(s).

Claims 25-30, 36, 43, 50, 57, 58, are so broad as to encompass any amylase comprising the modifications at the above mentioned three positions and having 80% through 97% identity to SEQ ID NO: 12. The scope of the claims is not commensurate with the enablement provided by the disclosure with regard to the extremely large number of amylases broadly encompassed by the claims. Since the amino acid sequence of a protein determines its structural and functional properties, predictability of which changes can be tolerated in a protein's amino acid sequence and obtain the desired activity requires a knowledge of and guidance with regard to which amino acids in the protein's sequence, if any, are tolerant of modification and which are conserved (i.e. expectedly intolerant to modification), and detailed knowledge of the ways in which the proteins' structure relates to its function. However, in this case the disclosure is limited to the variant amino acid sequence of only SEQ ID NO:12 selected from the group of alterations to amino acid at positions 118, 320 or 458 and wherein the alteration specifically comprises replacing the amino acid at said positions with lysine (K). It would require undue experimentation of the skilled artisan to make and use the claimed polypeptides. The specification is limited to teaching the use of SEQ ID NO: 12 with the any one of the above three amino acid modifications as a amylase but provides no guidance with regard to the making of variants and mutants that are 80% to 97% identical to SEQ ID NO 12 or with regard to other uses. In view of the great breadth of the claim, amount of experimentation required to make the

claimed polypeptides, the lack of guidance, working examples, and unpredictability of the art in predicting function from a polypeptide primary structure (e.g., see Ngo et al. in The Protein Folding Problem and Tertiary Structure Prediction, 1994, Merz et al. (ed.), Birkhauser, Boston, MA, pp. 433 and 492-495), the claimed invention would require undue experimentation. As such, the specification fails to teach one of ordinary skill how to use the full scope of the polypeptides encompassed by this claim.

While enzyme isolation techniques, recombinant and mutagenesis techniques are known, and it is routine in the art to screen for multiple substitutions or multiple modifications as encompassed by the instant claims, the specific amino acid positions within a protein's sequence where amino acid modifications can be made with a reasonable expectation of success in obtaining the desired activity/utility are limited in any protein and the result of such modifications is unpredictable. In addition, one skilled in the art would expect any tolerance to modification for a given protein to diminish with each further and additional modification, e.g. multiple substitutions.

The specification does not support the broad scope of the claims which encompass all modifications and fragments of any amylase with 80% through 97% identity to SEQ ID NO: 12, because the specification does not establish: (A) regions of the protein structure which may be modified without affecting amylase activity; (B) the general tolerance of amylases to modification and extent of such tolerance; (C) a rational and predictable scheme for modifying any amino acid residue with an expectation of obtaining the desired biological function; and (D) the specification provides insufficient guidance as to which of the essentially infinite possible choices is likely to be successful.

Thus, applicants have not provided sufficient guidance to enable one of ordinary skill in the art to make and use the claimed invention in a manner reasonably correlated with the scope of the claims broadly including amylases with an enormous number of amino acid modifications to SEQ ID NOS: 12. The scope of the claims must bear a reasonable correlation with the scope of enablement (*In re Fisher*, 166 USPQ 19 24 (CCPA 1970)). Without sufficient guidance, determination of polypeptides having the desired biological characteristics is unpredictable and the experimentation left to those skilled in the art is unnecessarily, and improperly, extensive and undue. See *In re Wands* 858 F.2d 731, 8 USPQ2nd 1400 (Fed. Cir, 1988).

In response to the previous Office action, applicant has traversed the above rejection arguing that the amended claims are directed to variants having a high degree of homology to SEQ ID NO:12 and that the specification describes many α amylases falling within the claimed invention . Applicant provides few examples of such variants. Applicant also argues that the specification provides working examples of α amylases which are at least 80% homologous to SEQ ID NO:12 and provides table suggesting specific amino acid changes. Applicant also argues that the specification describes methods which are well known in the art for practicing the invention and three dimensional structures of α amylases and methods to determine the conserved sequences. Examiner respectfully disagrees with such an argument as being persuasive to overcome the above rejection. First of all it must be recognized that applicant does not disclose or describe all those sequences that are 80% homologous to SEQ ID NO:12, even though the specification does indicate few specific variants. Furthermore, while methods to produce variants of a known sequence such as site-specific mutagenesis, random mutagenesis, etc. are well known to the skilled artisan, producing variants as claimed by applicants requires

that one of ordinary skill in the art know or be provided with guidance for the selection of which of the infinite number of variants have the claimed property. Instant claims sequences that are 80% through 97% identical to SEQ ID NO:12. Thus, in order to make the full scope of recited polypeptides, one skilled in the art has to modify up to approximately 20% of the nucleotides of the sequence of SEQ ID NO:12, comprising 485 amino acids. As noted in the Office action, the polypeptide variants encompass those having a single amino acid substitution, addition, deletion, or insertion and any combination of amino acid substitutions, additions, deletions, and/or insertions. Although the claims are not limited to variants having only a single amino acid substitution, in order to generate for example, only single amino acid variants of each amino acid of SEQ ID NO:12, one must make 19^{485} variants – just for *single amino acid variants*. Thus, at a minimum, the number of variants is 19^{485} and the number becomes seemingly infinite when one considers that the claims broadly encompass simultaneous other alterations by substitution, addition, deletion, and/or insertion. Therefore, while methods to produce variants of a known sequence, e.g., site-specific mutagenesis and random mutagenesis, are well-known to the skilled artisan, producing the claimed variants requires that one of skill in the art know or be provided with guidance for the selection of which of the at least 19^{485} variants has the desired activity. Without such guidance one of ordinary skill would be reduced to the necessity of producing and testing all of the at least 19^{485} possible variants. The art clearly *does not* typically engage in the screening of 19^{485} single amino acid variants and it follows that the art does not typically engage in the screening of $>19^{485}$ variants to isolate those relatively few variants that would have the desired activity. This would clearly constitute undue experimentation. While enablement is not precluded by the necessity for routine screening, if a large amount of screening is required, the

specification must provide a reasonable amount of guidance with respect to the direction in which the experimentation should proceed. Such guidance has not been provided in the instant specification. As such, based on a determination by weighing all of the factual considerations of In re Wands, the examiner has made a determination that the specification does not enable the claimed invention without undue experimentation. Hence the above rejection is maintained.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 25, 27, 30, 36, are rejected under 35 U.S.C. 102(b) as being anticipated by Igarashi et al. (Database SPTREMBL, Accession No. O82839, Nov. 1998). This rejection is based upon the public availability of an amino acid sequence. Claims 25, 27, 30, 36 of the instant application are drawn to a variant amylase polypeptide wherein said variant has amino acid K corresponding to the position 320 and wherein said polypeptide is at least 80%, identical to SEQ ID NO: 12. Igarashi et al. disclose such an amylase polypeptide which is 89% identical to SEQ ID NO comprising the amino acid K at a position corresponding to 320 of SEQ ID NO:12(see enclosed sequence alignment). Therefore Igarashi et al. anticipate claims 25, 27, 30, 36 of this application as written.

In response to the previous Office action, applicant has traversed the above rejection arguing that Igarashi et al. does not disclose substitution of a lysine at position 320, rather the

enzyme disclosed by Igarashi et al. has no alteration at position 320. Examiner respectfully disagrees with such an argument. It can be seen from the sequence alignment with SEQ ID NO:12, that the position corresponding to amino acid 320 is different from that in SEQ ID NO:12 and the modification is a change to amino acid "K" as claimed herein. Therefore, the above rejection is maintained.

Conclusion

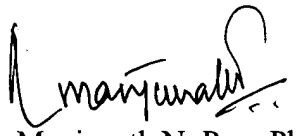
None of the claims are allowable.

THIS ACTION IS MADE FINAL. Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of this final action.

Any inquiry concerning this communication or earlier communications from the Examiner should be directed to Manjunath N. Rao, Ph.D. whose telephone number is 571-272-0939. The Examiner can normally be reached on 7.00 a.m. to 3.30 p.m. If attempts to reach the

examiner by telephone are unsuccessful, the Examiner's supervisor, Ponnathapura Achutamurthy can be reached on 571-272-0928. The fax phone numbers for the organization where this application or proceeding is assigned is 703-872-9306/9307 for regular communications and for After Final communications. Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is 571-272-1600.



Manjunath N. Rao, Ph.D.
Primary Examiner
Art Unit 1652

July 12, 2005

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 6, 2004, 23:59:28 ; Search time 46.501 Seconds
(without alignments)
3290.816 Million cell updates/sec

Title: US-09-925-576C-12
Perfect score: 2708
Sequence: 1 HHNGTNGTMMQYFEWYLPND.....ADGWGNPSVNGGSVSIWVNK 485

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2409	89.0	516	2	O82839	O82839 bacillus sp
2	1942	71.7	533	2	Q9AQ54	Q9aq54 bacillus me
3	1934	71.4	513	16	Q81YJ4	Q81yj4 bacillus an
4	1926	71.1	513	16	Q81AS4	Q81as4 bacillus ce
5	1889.5	69.8	613	2	Q59222	Q59222 bacillus sp
6	1874	69.2	519	2	Q9RQT8	Q9rqt8 cytophaga s
7	1872.5	69.1	549	2	O31193	O31193 bacillus st
8	1867.5	69.0	521	2	P71034	P71034 bacillus sp
9	1867.5	69.0	549	2	Q9KWY6	Q9kwy6 bacillus st
10	1813.5	67.0	501	2	Q93I48	Q93i48 bacillus sp
11	1576.5	58.2	507	16	Q87HG6	Q87hg6 vibrio para
12	1363	50.3	493	2	Q03657	Q03657 bacillus ci
13	1336	49.3	481	16	Q89YP1	Q89yp1 bacteroides
14	1307.5	48.3	486	16	Q8DT08	Q8dt08 streptococc
15	1307.5	48.3	488	16	Q8E0M2	Q8e0m2 streptococc
16	1300.5	48.0	488	16	Q8E696	Q8e696 streptococc
17	1298	47.9	484	16	Q97Q49	Q97q49 streptococc
18	1296	47.9	484	16	Q8DPC8	Q8dpc8 streptococc
19	1282	47.3	492	16	Q8YUZ1	Q8yuz1 anabaena sp
20	1279.5	47.2	486	2	O68875	O68875 streptococc
21	1262.5	46.6	484	2	O50583	O50583 streptococc
22	1260.5	46.5	485	2	Q53786	Q53786 streptococc
23	1148	42.4	491	16	Q9CG59	Q9cg59 lactococcus
24	1114	41.1	506	16	Q8U916	Q8u916 agrobacteri
25	1098	40.5	494	16	Q8Z5S5	Q8z5s5 salmonella
26	1085	40.1	495	16	Q8XBB6	Q8xbb6 escherichia
27	1080	39.9	495	16	Q8FGL8	Q8fgl8 escherichia
28	1073	39.6	495	16	C7UAB0	Q7uab0 shigella fl
29	1071	39.5	495	16	Q83R40	Q83r40 shigella fl
30	1048.5	38.7	529	3	Q877B1	Q877b1 aspergillus
31	494.5	18.3	461	1	O33476	O33476 pyrococcus
32	494.5	18.3	461	1	Q8NKR4	Q8nkr4 thermococcu
33	475.5	17.6	461	1	Q8NKR5	Q8nkr5 thermococcu
34	467	17.2	469	1	O50200	O50200 thermococcu
35	462.5	17.1	460	1	Q9P9L0	Q9p9l0 pyrococcus
36	462.5	17.1	460	1	O08452	O08452 pyrococcus
37	462.5	17.1	473	17	Q8U3I9	Q8u3i9 pyrococcus
38	459	16.9	432	14	Q8JZK3	Q8jzk3 uncultured
39	444	16.4	457	1	O93647	O93647 thermococcu
40	320.5	11.8	482	2	Q60051	Q60051 thermoactin
41	284.5	10.5	421	10	Q7X9T1	Q7x9t1 phaseolus a
42	280	10.3	423	10	Q42678	Q42678 cuscuta ref
43	280	10.3	504	1	Q60224	Q60224 natronococc
44	279	10.3	416	10	Q8LJQ6	Q8ljq6 musa acumin
45	278	10.3	424	10	Q8LP27	Q8lp27 pharbitis n

ALIGNMENTS

RESULT 1
O82839
ID O82839 PRELIMINARY; PRT; 516 AA.
AC O82839;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amylase.
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KSM-1378;
RX MEDLINE=98342096; PubMed=9675143;
RA Igarashi K., Hatada Y., Ikawa K., Araki H., Ozawa T., Kobayashi T.,
RA Ozaki K., Ito S.;
RT "Improved thermostability of a Bacillus alpha-amylase by deletion of
RT an arginine-glycine residue is caused by enhanced calcium binding.";
RL Biochem. Biophys. Res. Commun. 248:372-377(1998).
DR EMBL; AB008763; BAA32431.1; -.
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Aamy; 1.
SQ SEQUENCE 516 AA; 58841 MW; D90A8C90ECC182F8 CRC64;

Query Match 89.0%; Score 2409; DB 2; Length 516;
Best Local Similarity 86.0%; Pred. No. 5.9e-143;
Matches 417; Conservative 37; Mismatches 31; Indels 0; Gaps 0;

```
Qy          1 HHNGTNGTMMQYFEWYLPNDGNHWNRLRSDASNLKDKGISAVWIPPAWKGASQNDVGYGA 60
              |||||||||||||||:|||||||||||| ||:||| |||:|||||||||| |||||||||
Db         32 HHNGTNGTMMQYFEWHLPNDGNHWNRLRDDAANLKSKGITAVWIPPAWKGTSQNDVGYGA 91
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               ||||||||||||||:|||||||:||| || :||:||||||||||||||||||| |||| ||
Db          92 YDLYDLGEFNQKGTVRTKYGTRSQLQGAVTSLKNNGIQVYGDVVMNHKGGADGTEMVNAV 151

Qy         121 EVNPNNRNQEVSGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGVDWDQSRKLNNRIYKF 180
               ||| :||||||:|||||||||||||||||||||||||||||||||||| ||||||:| |:||||
Db         152 EVNRSNRNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKF 211

Qy         181 RGDGKGWDWEVDTENGNYDYLMYADIDMDHPEVVNELRNWGVWYTNTLGLDGFRIDAVKH 240
               || || |||||| ||||||||||||||||||||:|||||||||||||| ||||||||||
Db         212 RGTGKAWDWEVDIENGNYDYLMYADIDMDHPEVINELRNWGVWYTNTLNLDGFRIDAVKH 271

Qy         241 IKYSFTRDWINHVRSATGKNMFAVAEFWKNDLGAIENYLNKTNWNHSVFDVPLHYNLYNA 300
               ||||:||||: |||: ||| |||||||||||| ||||||||:|||||||||||||||||
Db         272 IKYSYTRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNA 331

Qy         301 SKSGGNYDMRQIFNGTVVQRHPMHAVTFVDNHDSQPEEALESFVEEWFKPLAYALTLTRE 360
               | ||| :||| | ||:|||:||:|||||||||||||| ||||||| |||||||| ||||
Db         332 SNSGGYFDMRNILNGSVVQKHPIHAVTFVDNHDSQPGEALESFVQSWFKPLAYALILTRE 391

Qy         361 QGYPSVFYGDYYGIPTHGVPAMKSKIDPILEARQKYAYGRQNDYLDHHNIIGWTREGNTA 420
               ||||||||||||||||||:|||||||:|:||| |||| |:|| |||:|||||||:::
Db         392 QGYPSVFYGDYYGIPTHGVPSMKSKIDPLLQARQTYAYGTQHDYFDHHDIIGWTREGDSS 451

Qy         421 HPNSGLATIMSDGAGGNKWMFVGRNKAGQVWTDITGNRAGTVTINADGWGNFSVNGGSVS 480
               |||||||||||| |||||:||::|||||| ||||||:||||||||||||:||||:||
Db         452 HPNSGLATIMSDGPGGNKWMYVGKHKAGQVWRDITGNRSGTVTINADGWGNFTVNGGAVS 511

Qy         481 IWVNK 485
                :|| :
Db         512 VWVKQ 516
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RESULT 2
Q9AQ54
ID Q9AQ54 PRELIMINARY; PRT; 533 AA.
AC Q9AQ54;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-W.,
RA Park K.-H.;
RT "Cloning of maltopentaose-producing amylase from Bacillus megaterium
RT KSM B-404.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF220440; AAK00598.1; -.
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Aamy; 1.
SQ SEQUENCE 533 AA; 60557 MW; 789CECD6A19C7DDE CRC64;

Query Match 71.7%; Score 1942; DB 2; Length 533;
Best Local Similarity 69.6%; Pred. No. 1.1e-113;
Matches 336; Conservative 57; Mismatches 86; Indels 4; Gaps 2;

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Qy           6 NGTMMQYFEWYLPNDGNHWNRLRSDASNLKDKGISAVWIPPAWKGASQNDVGYGAYDLYD 65
               |||:|||||| ||||||||||:|| || |||::||||||:|| :|||||||||||||
Db          52 NGTLMQYFEWYAPNDGNHWNRLRTDAENLAQKGITSVWIPPAYKGTTQNDVGYGAYDLYD 111

Qy          66 LGEFNQKGTIRTKYGTRNQLQAAVNALKSNGIQVYGDVVMNHKGGADATEMVRAVEVNPN 125
               |||||||||:|||||: ||::|::||    | ||||||||||||| || | ||||:|:
Db         112 LGEFNQKGTVRTKYGTKAQLKSAIDALHKKNIDVYGDVVMNHKGGADYTETVTAVEVDPS 171
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Qy         126 NRNQEVSGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGVDWDQSRKLNNRIYKFRGDGK 185
               ||| |||||| | ||| |:|||||:::|||||:|||||| |||: ||| |||||||| ||
Db         172 NRNVEVSGDYEISAWTGFNFPGRGDSYSNFKWKWYHFDGTDWDEGRKL-NRIYKFRGIGK 230

Qy         186 GWDWEVDTENGNYDYLMYADIDMDHPEVVNELRNWGVWYTNTLGLDGFRIDAVKHIKYSF 245
               ||||| :|||||||||||:| |||:| ||:: || || | | |||||:|||||| : :
Db         231 AWDWEVSSENGNYDYLMYADLDFDHPDVANEMKKWGTWYANELNLDGFRLDAVKHIDHEY 290

Qy         246 TRDWINHVRSATGKNMFAVAEFWKNDLGAIENYLNKTNWNHSVFDVPLHYNLYNASKSGG 305
               |||:|||| ||| ||||||:|:||:  : ||| | |:| |||| ||||| : |||  |
Db         291 LRDWVNHVRQQTGKEMFAVAEYWQNDIQTLNNYLAKVNYNQSVFDAPLHYNFHYASKGNG 350

Qy         306 NYDMRQIFNGTVVQRHPMHAVTFVDNHDSQPEEALESFVEEWFKPLAYALTLTREQGYPS 365
               ||||| |  |||| ||  ||| |:|||||| ::||| |  |||||||  ||| :||||
Db         351 NYDMRNILKGTVVANHPTLAVTLVENHDSQPGQSLESVVSPWFKPLAYAFILTRAEGYPS 410

Qy         366 VFYGDYYGI---PTHGVPAMKSKIDPILEARQKYAYGRQNDYLDHHNIIGWTREGNTAHP 422
               ||||||||      : :||:| |||||| ||: |||| | || || ::||||||:: |
Db         411 VFYGDYYGTKGNSNYEIPALKDKIDPILTARKNYAYGTQRDYFDHPDVIGWTREGDSVHA 470

Qy         423 NSGLATIMSDGAGGNKWMFVGRNKAGQVWTDITGNRAGTVTINADGWGNFSVNGGSVSIW 482
               ||||||:|||| || ||| ||:| ||::| |||||:  |||||  |||| | |:|||||:
Db         471 NSGLATLISDGPGGAKWMDVGKNNAGEIWYDITGNQTNTVTINKDGWGQFQVSGGSVSIY 530

Qy         483 VNK 485
               | :
Db         531 VQR 533
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RESULT 3
Q81YJ4
ID Q81YJ4 PRELIMINARY; PRT; 513 AA.
AC Q81YJ4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase.
GN AMYS OR BA3551.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
DR EMBL; AE017035; AAP27311.1; -.
DR TIGR; BA3551; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Aamy; 1.
KW Complete proteome.
SQ SEQUENCE 513 AA; 58445 MW; 558D6EF282FD159B CRC64;

Query Match 71.4%; Score 1934; DB 16; Length 513;
Best Local Similarity 69.4%; Pred. No. 3.4e-113;
Matches 335; Conservative 59; Mismatches 85; Indels 4; Gaps 2;